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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=14; hr=11; min=59; sec=22; ms=702; ]

=====

\*\*\*\*\*

Reviewer Comments:

SEQUENCE LISTING

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND  
TECHNOLOGY  
MIYAKE, Masato  
YOSHIKAWA, Tomohiro  
UCHIMURA, Eiichiro  
MIYAKE, Jun

<120> COMPOSITION AND METHOD FOR INCREASING EFFICIENCY OF INTRODUCTION  
OF TARGET SUBSTANCE INTO CELL

The above <120> response exceeds the Sequence Rules' required 72-  
character line limit. Please adjust the lines.

<210> 14  
<211> 1798  
<212> DNA  
<213> Artificial

<220>  
<223> pcr fragment

The above <223> response is an insufficient explanation for  
"Artificial": please give more information regarding the source of the  
genetic material. Same error in Sequences 15 through 18.

\*\*\*\*\*



Application No: 10594349 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2008-04-14 10:58:24.861  
**Finished:** 2008-04-14 10:58:28.767  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 906 ms  
**Total Warnings:** 7  
**Total Errors:** 12  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)



# SEQUENCE LISTING

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND  
TECHNOLOGY  
MIYAKE, Masato  
YOSHIKAWA, Tomohiro  
UCHIMURA, Eiichiro  
MIYAKE, Jun

<120> COMPOSITION AND METHOD FOR INCREASING EFFICIENCY OF INTRODUCTION OF TARGET SUBSTANCE  
INTO CELL

<130> AI003PCT

<140> 10594349

<141> 2008-04-14

<150> JP2003-057869

<151> 2003-03-04

<160> 18

<210> 1

<211> 1929

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1929)

<223> fibronectin 1

<400> 1

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ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag	96
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln	
20 25 30	

gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc	144
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser	
35 40 45	

aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag	192
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln	
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tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga	240
Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly	
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gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act	288
Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr	
85 90 95	

tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat	336
Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr	
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 gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg gct	384
Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala	
115 120 125	
 ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa ggg	432
Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly	
130 135 140	
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Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr	
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Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu	
165 170 175	
 tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct ggg	576
Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly	
180 185 190	
 act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc tgg	624
Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp	
195 200 205	
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Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr	
210 215 220	
 tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc tat	720
Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr	
225 230 235 240	
 aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg ctc	768
Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu	
245 250 255	
 cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag agg	816
Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg	
260 265 270	
 cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc gat	864
His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp	
275 280 285	
 gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct ccc	912
Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro	
290 295 300	
 tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg atg	960
Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met	
305 310 315 320	

cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc ctg	1008
Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu	
325 330 335	
ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt	1056
Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly	
340 345 350	
ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat ggc	1104
Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly	
355 360 365	
agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct	1152
Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser	
370 375 380	
ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc	1200
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser	
385 390 395 400	
aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac	1248
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr	
405 410 415	
act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg	1296
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly	
420 425 430	
acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg	1344
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met	
435 440 445	
gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc	1392
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg	
450 455 460	
att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg	1440
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg	
465 470 475 480	
tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac	1488
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr	
485 490 495	
tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg	1536
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val	
500 505 510	
aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt	1584
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys	
515 520 525	
aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac	1632
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp	
530 535 540	
caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca	1680

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser  
 545 550 555 560

tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc 1728  
 Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly  
 565 570 575

cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc 1776  
 Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser  
 580 585 590

tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc 1824  
 Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro  
 595 600 605

aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc 1872  
 Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser  
 610 615 620

aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt 1920  
 Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu  
 625 630 635 640

gga tac tga 1929  
 Gly Tyr

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 <211> 642  
 <212> PRT  
 <213> Homo sapiens

<400> 2

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 35 40 45

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
 50 55 60

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 65 70 75 80

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
 85 90 95



Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
100 105 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
165 170 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
180 185 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
195 200 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
210 215 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
225 230 235 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
245 250 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
260 265 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
275 280 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro  
290 295 300

Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met  
305 310 315 320

Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu  
325 330 335

Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly  
340 345 350

Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly  
355 360 365

Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser  
370 375 380

Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser  
385 390 395 400

Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr  
405 410 415

Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly  
420 425 430

Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met  
435 440 445

Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg  
450 455 460

Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg  
465 470 475 480

Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr  
485 490 495

Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val  
500 505 510

Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys  
515 520 525

Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp  
530 535 540

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser  
 545 550 555 560

Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly  
 565 570 575

Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser  
 580 585 590

Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro  
 595 600 605

Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser  
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Gly Tyr

<210> 3  
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 <213> Mus musculus

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 <222> (1)..(1437)  
 <223> vitronectin

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 tct ctg gct gac caa gag tca tgc aag ggc cgc tgc act cag ggt ttc 96  
 Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe  
 20 25 30  
 atg gcc agc aag aag tgt cag tgt gac gag ctt tgc act tac tat cag 144  
 Met Ala Ser Lys Lys Cys Gln Cys Asp Glu Leu Cys Thr Tyr Tyr Gln  
 35 40 45  
 agc tgc tgt gcc gac tac atg gag cag tgc aag ccc caa gta acg cgg 192  
 Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg  
 50 55 60

[illegible]